

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kwon, Byoung Se
- (ii) TITLE OF INVENTION: New Receptor and Related Products and Methods
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Barnard, Brown & Michaels
(B) STREET: 306 East State Street, Suite 220
(C) CITY: Ithaca
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 14850
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- a4 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/422,796
(B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/012,269
(B) FILING DATE: 01-FEB-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/922,996
(B) FILING DATE: 30-JUL-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/267,577
(B) FILING DATE: 07-NOV-1988
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Michaels, Christopher A
(B) REGISTRATION NUMBER: 34,390
(C) REFERENCE/DOCKET NUMBER: KWO4
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 607-273-1711
(B) TELEFAX: 607-273-2609

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (C) INDIVIDUAL ISOLATE: H4-1BB #1
- (D) DEVELOPMENTAL STAGE: Differentiated T-cell
- (G) CELL TYPE: Lymphocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..805
- (D) OTHER INFORMATION: /codon_start= 41

/product= "H4-1BB"

/number= 1

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 41..802
- (D) OTHER INFORMATION: /codon_start= 41

/product= "H4-1BB"

/number= 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ay
ent.

AATCAGCTTT GCTAGTATCA TACCTGTGCC AGATTTCATC ATG GGA AAC AGC TGT	55
Met Gly Asn Ser Cys	
1 5	
TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC AAC TTT GAG AGG ACA	103
Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu Asn Phe Glu Arg Thr	
10 15 20	
AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA GCT GGT ACA TTC TGT	151
Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys	
25 30 35	
GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT CCT CCA AAT AGT TTC	199
Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe	
40 45 50	
TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA TGC AGG CAG TGT AAA	247
Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys	
55 60 65	
GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC ACC AGC AAT GCA GAG	295
Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu	
70 75 80 85	
TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG GCA GGA TGC AGC ATG	343
Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met	

90

95

100

TGT	GAA	CAG	GAT	TGT	AAA	CAA	GGT	CAA	GAA	CTG	ACA	AAA	AAA	GGT	TGT	391
Cys	Glu	Gln	Asp	Cys	Lys	Gln	Gly	Gln	Glu	Leu	Thr	Lys	Lys	Gly	Cys	
			105					110						115		
AAA	GAC	TGT	TGC	TTT	GGG	ACA	TTT	AAC	GAT	CAG	AAA	CGT	GGC	ATC	TGT	439
Lys	Asp	Cys	Cys	Phe	Gly	Thr	Phe	Asn	Asp	Gln	Lys	Arg	Gly	Ile	Cys	
		120					125					130				
CGA	CCC	TGG	ACA	AAC	TGT	TCT	TTG	GAT	GGA	AAG	TCT	GTG	CTT	GTG	AAT	487
Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Lys	Ser	Val	Leu	Val	Asn	
	135					140					145					
GGG	ACG	AAG	GAG	AGG	GAC	GTG	GTC	TGT	GGA	CCA	TCT	CCA	GCT	GAC	CTC	535
Gly	Thr	Lys	Glu	Arg	Asp	Val	Val	Cys	Gly	Pro	Ser	Pro	Ala	Asp	Leu	
150					155					160					165	
TCT	CCG	GGA	GCA	TCC	TCT	GTG	ACC	CCG	CCT	GCC	CCT	GCG	AGA	GAG	CCA	583
Ser	Pro	Gly	Ala	Ser	Ser	Val	Thr	Pro	Pro	Ala	Pro	Ala	Arg	Glu	Pro	
				170					175					180		
GGA	CAC	TCT	CCG	CAG	ATC	ATC	TCC	TTC	TTT	CTT	GCG	CTG	ACG	TCG	ACT	631
Gly	His	Ser	Pro	Gln	Ile	Ile	Ser	Phe	Phe	Leu	Ala	Leu	Thr	Ser	Thr	
			185					190					195			
GCG	TTG	CTC	TTC	CTG	CTG	TTC	TTC	CTC	ACG	CTC	CGT	TTC	TCT	GTT	GTT	679
Ala	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Thr	Leu	Arg	Phe	Ser	Val	Val	
		200					205					210				
AAA	CGG	GGC	AGA	AAG	AAA	CTC	CTG	TAT	ATA	TTC	AAA	CAA	CCA	TTT	ATG	727
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	
	215					220					225					
AGA	CCA	GTA	CAA	ACT	ACT	CAA	GAG	GAA	GAT	GGC	TGT	AGC	TGC	CGA	TTT	775
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	
230					235					240					245	
CCA	GAA	GAA	GAA	GAA	GGA	GGA	TGT	GAA	CTG	TGAAATGGAA	GTCAATAGGG					825
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu							
				250					255							
CTGTTGGGAC	TTT															838

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Asn	Ser	Cys	Tyr	Asn	Ile	Val	Ala	Thr	Leu	Leu	Leu	Val	Leu	
1				5					10					15		
Asn	Phe	Glu	Arg	Thr	Arg	Ser	Leu	Gln	Asp	Pro	Cys	Ser	Asn	Cys	Pro	

20

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Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
 65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
 85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
 100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
 115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
 130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
 145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
 165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
 180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
 195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
 210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
 225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTYTGYMGAA ARTAYAAAYCC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTYTCSTSCA HTGGTGGACA

20

(2) INFORMATION FOR SEQ ID NO:5:

*at
ant.*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCARGSWRC AGGTYTTRCA

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTYTGRTCRT TRAATGTTCC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

a4
anal. (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATAAGCTTT GCTAGTATCA TACCT

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTAAGATCTC TGCGGAGAGT GTCCTGGCTC

30